What is claimed is:

1. A method of identifying *Campylobacter jejuni* strains in a sample suspected of containing *Campylobacter jejuni* DNA by polymerase chain reaction, wherein the amplification products of said polymerase chain reaction are derived from genes within the *Campylobacter jejuni* polysaccharide capsule (CPS) loci, comprising: (a) subjecting DNA from said sample to a PCR amplification reaction using one or more PCR primer pairs targeting one or more regions of the O-methyl phosphoramidate synthesis region, heptose synthesis and hyper-variable region of the polysaccharide capsule loci of *Camplylobacter jejuni*; (b) analyzing amplification products resulting from said amplification reaction.

2. The method of claim 1, wherein said polysaccharide capsule loci is derived from *Campylobacter jejuni* strains selected from HS2; HS3; HS6; HS10; HS15C; HS41; HS53; HS1; HS23; HS42; HS44; HS17 and strain 8486.

3. The method of claim 2, wherein said HS2 PCR primers recognize HS2 Penner type; HS3 PCR primers recognize H3 Penner type; HS4 PCR primers recognize HS4 A Penner complex; HS6 PCR primers recognize HS6 Penner type; HS 10 PCR primers recognize HS10 Penner type; HS15C PCR primers recognize HS15 and HS31 Penner types; HS41 PCR primers recognize HS41 Penner type; HS53 PCR primers recognize HS53 Penner type; HS1D PCR primers recognize HS1 complex Penner type; HS17 PCR primers recognize HS8 and HS17 Penner type; 8486 PCR primers recognize HS4B Penner type; HS23 PCR primers recognize HS23 Penner complex; HS42E PCR primers recognize HS42 Penner type; HS44 PCR primers recognize HS44 Penner type.

4. The method of claim 1, wherein said amplification products are analyzed by size determination.

5. The method of claim 4, wherein the amplification of products are analyzed by agarose gel electrophoresis.

6. The method of claim 1, wherein said PCR primer pairs contain sequences selected from the group consisting of: SEQ ID NO: 1 and SEQ ID NO: 2; SEQ ID NO: 3 and SEQ ID NO: 4; SEQ ID NO: 5 and SEQ ID NO: 6; SEQ ID NO: 7 and SEQ ID NO: 8; SEQ ID NO: 9 and SEQ ID NO: 10; SEQ ID NO: 11 and SEQ ID NO: 12; SEQ ID NO: 13 and SEQ ID NO: 14; SEQ ID NO: 15 and SEQ ID NO: 16; SEQ ID NO: 17 and SEQ ID NO: 18; SEQ ID NO: 19 and SEQ ID NO: 20; SEQ ID NO: 21 and SEQ ID NO: 22; SEQ ID NO: 23 and SEQ ID NO: 24; SEQ ID NO: 25 and SEQ ID NO: 26; SEQ ID NO 27 and SEQ ID NO: 28.

7. The method of claim 1, wherein said PCR reaction is multiplex amplification reaction.

8. The method of claim 7, wherein said PCR primer pairs are grouped into an alpha mix comprising one or more sequence pairs selected from the group consisting of: SEQ ID NO: 1 and SEQ ID NO: 2; SEQ ID NO: 3 and SEQ ID NO: 4; SEQ ID NO: 5 and SEQ ID NO: 6; SEQ ID NO: 7 and SEQ ID NO: 8; SEQ ID NO: 9 and SEQ ID NO: 10; SEQ ID NO: 11 and SEQ ID NO: 12; SEQ ID NO: 13 and SEQ ID NO: 14; SEQ ID NO: 15 and SEQ ID NO: 16, and a beta mix comprising one or more sequence pairs selected from the group consisting of: SEQ ID NO: 17 and SEQ ID NO: 18; SEQ ID NO: 19 and SEQ ID NO: 20; SEQ ID NO: 21 and SEQ ID NO: 22; SEQ ID NO: 23 and SEQ ID NO: 24; SEQ ID NO: 25 and SEQ ID NO: 26; SEQ ID NO 27 and SEQ ID NO: 28.

9. The method of claim 1, wherein said primer pairs are grouped in order to discriminate PCR amplification reaction product sizes.

10. The method of claim 1, wherein said sample is a clinical sample.

11. The method of claim 1, wherein said sample is collected from a matrix selected from the group consisting of a bacterial culture, a blood, a tissue, and fecal material.

12. The method of claim 1, wherein the primers have about 18-30 nucleotides, a G/C content of 20-50%, and a melting temperature between about 57° C. and 63° C.

13. The method of claim 1, wherein said amplification reaction yields one or more of amplification products selected from the group consisting of SEQ ID NO: 29; SEQ ID NO: 30; SEQ ID NO: 31; SEQ ID NO: 32; SEQ ID NO: 33; SEQ ID NO: 34; SEQ ID NO: 35; SEQ ID NO: 36; SEQ ID NO: 37; SEQ ID NO: 38; SEQ ID NO: 39; SEQ ID NO: 40; SEQ ID NO: 41; and SEQ ID NO: 42.

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